

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Berlin, Vivian
Chiu, Isabel

10

(ii) TITLE OF INVENTION:

(iii) NUMBER OF SEQUENCES: 25

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

20

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (text)

25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

30

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709
(C) REFERENCE/DOCKET NUMBER: MII-036CP

35

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
(B) TELEFAX: (617) 227-5941

40

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA

55

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	CTC ACC CGT CAC AAT GCA GCC AAC AAG ATC TTG AAG AAC ATG TGT GAA Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu 1 5 10 15	48
10	CAC AGC AAC ACG CTG GTC CAG CAG GCC ATG ATG GTG AGT GAA GAG CTG His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu 20 25 30	96
15	ATT CGG GTA GCC ATC CTC TGG CAT GAG ATG TGG CAT GAA GGC CTG GAA Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu 35 40 45	144
20	GAG GCA TCT CGC TTG TAC TTT GGG GAG AGG AAC GTG AAA GGC ATG TTT Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe 50 55 60	192
25	GAG GTG CTG GAG CCC CTG CAT GCT ATG ATG GAA CGG GGT CCC CGG ACT Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr 65 70 75 80	240
30	CTG AAG GAA ACA TCC TTT AAT CAG GCA TAT GGC CGA GAT TTA ATG GAG Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu 85 90 95	288
35	GCA CAA GAA TGG TGT CGA AAG TAC ATG AAG TCG GGG AAC GTC AAG GAC Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp 100 105 110	336
40	CTC ACG CAA GCC TGG GAC CTC TAC TAT CAC GTG TTC AGA CGG ATC TCA Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser 115 120 125	384
45	AAG CAG CTA CCC CAG CTC ACA TCC CTG GAG CTG CAG TAT GTG TCC CCC Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro 130 135 140	432
50	AAA CTT CTG ATG TGC CGA GAC CTT GAG TTG GCT GTG CCA GGA ACA TAC Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr 145 150 155 160	480
55	GAC CCC Asp Pro	486

(2) INFORMATION FOR SEQ ID NO:2:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
1 5 10 15

His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
5 20 25 30

Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
35 40 45

10 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
50 55 60

Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
65 70 75 80

15 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
85 90 95

20 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
100 105 110

Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
115 120 125

25 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
130 135 140

30 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
145 150 155 160

Asp Pro

35 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: other nucleic acid

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTTTGGAA TTCCTAATAA TGTCTGTACA AGTAGAAACC

40

50 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGTTTCGGG ATCCCGTCAT TCCAGTTTA CAAC

34

10 (2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 14..325

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 GGAATTCCTA ATA ATG TCC GTA CAA GTA GAA ACC ATC TCC CCA GGA GAC
Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp
1 5 10

49

30 GGG CGC ACC TTC CCC AAG CGC GGC CAG ACC TGC GTG GTG CAC TAC ACC
Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
15 20 25

97

35 GGG ATG CTT GAA GAT GGA AAG AAA TTT GAT TCC TCC CGT GAC CGT AAC
Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
30 35 40

145

40 AAG CCC TTT AAG TTT ATG CTA GGC AAG CAG GAG GTG ATC CGA GGC TGG
Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
45 50 55 60

193

45 GAA GAA GGG GTT GCC CAG ATG AGT GTG GGT CAG CGT GCC AAA CTG ACT
Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
65 70 75

241

50 ATA TCT CCA GAT TAT GCC TAT GGT GCC ACT GGG CAC CCA GGC ATC ATC
Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
80 85 90

289

55 CCA CCA CAT GCC ACT CTC GTC TTC GAT GTG GAG CTT CTAAACTGG
Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
95 100

335

AATGACGGGA TCC

348

55 (2) INFORMATION FOR SEQ ID NO:6:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1 5 10 15

20 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
20 25 30

25 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
35 40 45

30 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

35 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

40 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

45 Thr Leu Val Phe Asp Val Glu Leu
100

50

(2) INFORMATION FOR SEQ ID NO:7:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: other nucleic acid

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

50 TCGCCGGAAT TCGGGGGCGG AGGTGGAGGA GTACAAGTAG AAACCATC

48

55 (2) INFORMATION FOR SEQ ID NO:8:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 GGGTTTCGGG ATCCCGTCAT TCCAGTTTA GAAG

34

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 CGCGGATCCG CGCATTATTA CTTGTTTG A TTGATTTTT G

41

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

CGCGGATCCG CGTAAAAGCA AAGTACTATC AATTGAGCCG

40

(2) INFORMATION FOR SEQ ID NO:11:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

50

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..5427

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTG GAG CAC AGT GGG ATT GGA AGA ATC AAA GAG CAG AGT GCC CGC ATG
Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met

48

	1	5	10	15	
5	CTG GGG CAC CTG GTC TCC AAT GCC CCC CGA CTC ATC CGC CCC TAC ATG Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met 20 25 30				96
10	GAG CCT ATT CTG AAG GCA TTA ATT TTG AAA CTG AAA GAT CCA GAC CCT Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro 35 40 45				144
15	GAT CCA AAC CCA GGT GTG ATC AAT AAT GTC CTG GCA ACA ATA GGA GAA Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu 50 55 60				192
20	TTG GCA CAG GTT AGT GGC CTG GAA ATG AGG AAA TGG GTT GAT GAA CTT Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu 65 70 75 80				240
25	TTT ATT ATC ATC ATG GAC ATG CTC CAG GAT TCC TCT TTG TTG GCC AAA Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys 85 90 95				288
30	AGG CAG GTG GCT CTG TGG ACC CTG GGA CAG TTG GTG GCC AGC ACT GGC Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly 100 105 110				336
35	TAT GTA GTA GAG CCC TAC AGG AAG TAC CCT ACT TTG CTT GAG GTG CTA Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu 115 120 125				384
40	CTG AAT TTT CTG AAG ACT GAG CAG AAC CAG GGT ACA CGC AGA GAG GCC Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala 130 135 140				432
45	ATC CGT GTG TTA GGG CTT TTA GGG GCT TTG GAT CCT TAC AAG CAC AAA Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys 145 150 155 160				480
50	GTG AAC ATT GGC ATG ATA GAC CAG TCC CGG GAT GCC TCT GCT GTC AGC Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser 165 170 175				528
55	CTG TCA GAA TCC AAG TCA AGT CAG GAT TCC TCT GAC TAT AGC ACT AGT Leu Ser Glu Ser Lys Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser 180 185 190				576
60	GAA ATG CTG GTC AAC ATG GGA AAC TTG CCT CTG GAT GAG TTC TAC CCA Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro 195 200 205				624
65	GCT GTG TCC ATG GTG GCC CTG ATG CGG ATC TTC CGA GAC CAG TCA CTC Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu 210 215 220				672
70	TCT CAT CAT CAC ACC ATG GTT GTC CAG GCC ATC ACC TTC ATC TTC AAG Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys 225 230 235 240				720

	TCC CTG GGA CTC AAA TGT GTG CAG TTC CTG CCC CAG GTC ATG CCC ACG Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr 245 250 255	768
5	TTC CTT AAT GTC ATT CGA GTC TGT GAT GGG GCC ATC CGG GAA TTT TTG Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu 260 265 270	816
10	TTC CAG CAG CTG GGA ATG TTG GTG TCC TTT GTG AAG AGC CAC ATC AGA Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg 275 280 285	864
15	CCT TAT ATG GAT GAA ATA GTC ACC CTC ATG AGA GAA TTC TGG GTC ATG Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu Phe Trp Val Met 290 295 300	912
20	AAC ACC TCA ATT CAG AGC ACG ATC ATT CTT CTC ATT GAG CAA ATT GTG Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile Glu Gln Ile Val 305 310 315 320	960
25	GTA GCT CTT GGG GGT GAA TTT AAG CTC TAC CTG CCC CAG CTG ATC CCA Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro 325 330 335	1008
30	CAC ATG CTG CGT GTC TTC ATG CAT GAC AAC AGC CCA GGC CGC ATT GTC His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val 340 345 350	1056
35	TCT ATC AAG TTA CTG GCT GCA ATC CAG CTG TTT GGC GCC AAC CTG GAT Ser Ile Lys Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp 355 360 365	1104
40	GAC TAC CTG CAT TTA CTG CTG CCT CCT ATT GTT AAG TTG TTT GAT GCC Asp Tyr Leu His Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala 370 375 380	1152
45	CCT GAA GCT CCA CTG CCA TCT CGA AAG GCA GCG CTA GAG ACT GTG GAC Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp 385 390 395 400	1200
50	CGC CTG ACG GAG TCC CTG GAT TTC ACT GAC TAT GCC TCC CGG ATC ATT Arg Leu Thr Glu Ser Leu Asp Phe Thr Asp Tyr Ala Ser Arg Ile Ile 405 410 415	1248
55	CAC CCT ATT GTT CGA ACA CTG GAC CAG AGC CCA GAA CTG CGC TCC ACA His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu Leu Arg Ser Thr 420 425 430	1296
	GCC ATG GAC ACG CTG TCT TCA CTT GTT TTT CAG CTG GGG AAG AAG TAC Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu Gly Lys Lys Tyr 435 440 445	1344
	CAA ATT TTC ATT CCA ATG GTG AAT AAA GTT CTG GTG CGA CAC CGA ATC Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val Arg His Arg Ile 450 455 460	1392
	AAT CAT CAG CGC TAT GAT GTG CTC ATC TGC AGA ATT GTC AAG GGA TAC Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile Val Lys Gly Tyr	1440

	465	470	475	480	
5	ACA CTT GCT GAT GAA GAG GAG GAT CCT TTG ATT TAC CAG CAT CGG ATG Thr Leu Ala Asp Glu Glu Glu Asp Pro Leu Ile Tyr Gln His Arg Met	485	490	495	1488
10	CTT AGG AGT GGC CAA GGG GAT GCA TTG GCT AGT GGA CCA GTG GAA ACA Leu Arg Ser Gly Gln Gly Asp Ala Leu Ala Ser Gly Pro Val Glu Thr	500	505	510	1536
15	GGA CCC ATG AAG AAA CTG CAC GTC AGC ACC ATC AAC CTC CAA AAG GCC Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn Leu Gln Lys Ala	515	520	525	1584
20	TGG GGC GCT GCC AGG AGG GTC TCC AAA GAT GAC TGG CTG GAA TGG CTG Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp Leu Glu Trp Leu	530	535	540	1632
25	AGA CGG CTG AGC CTG GAG CTG CTG AAG GAC TCA TCA TCG CCC TCC CTG Arg Arg Leu Ser Leu Glu Leu Lys Asp Ser Ser Ser Pro Ser Leu	545	550	555	1680
30	CGC TCC TGC TGG GCC CTG GCA CAG GCC TAC AAC CCG ATG GCC AGG GAT Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro Met Ala Arg Asp	565	570	575	1728
35	CTC TTC AAT GCT GCA TTT GTG TCC TGC TGG TCT GAA CTG AAT GAA GAT Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu Leu Asn Glu Asp	580	585	590	1776
40	CAA CAG GAT GAG CTC ATC AGA AGC ATC GAG TTG GCC CTC ACC TCA CAA Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln	595	600	605	1824
45	GAC ATC GCT GAA GTC ACA CAG ACC CTC TTA AAC TTG GCT GAA TTC ATG Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu Ala Glu Phe Met	610	615	620	1872
50	GAA CAC AGT GAC AAG GGC CCC CTG CCA CTG AGA GAT GAC AAT GGC ATT Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp Asn Gly Ile	625	630	635	1920
55	GTT CTG CTG GGT GAG AGA GCT GCC AAG TGC CGA GCA TAT GCC AAA GCA Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala Tyr Ala Lys Ala	645	650	655	1968
60	CTA CAC TAC AAA GAA CTG GAG TTC CAG AAA GGC CCC ACC CCT GCC ATT Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro Thr Pro Ala Ile	660	665	670	2016
65	CTA GAA TCT CTC ATC AGC ATT AAT AAT AAG CTA CAG CAG CCG GAG GCA Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln Gln Pro Glu Ala	675	680	685	2064
70	GCG GCC GGA GTG TTA GAA TAT GCC ATG AAA CAC TTT GGA GAG CTG GAG Ala Ala Gly Val Leu Glu Tyr Ala Met Lys His Phe Gly Glu Leu Glu	690	695	700	2112

ATC CAG GCT ACC TGG TAT GAG AAA CTG CAC GAG TGG GAG GAT GCC CTT Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp Glu Asp Ala Leu 705	710	715	720	2160
5 GTG GCC TAT GAC AAG AAA ATG GAC ACC AAC AAG GAC GAC CCA GAG CTG Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp Asp Pro Glu Leu 725	730	735		2208
10 ATG CTG GGC CGC ATG CGC TGC CTC GAG GCC TTG GGG GAA TGG GGT CAA Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly Glu Trp Gly Gln 740	745	750		2256
15 CTC CAC CAG CAG TGC TGT GAA AAG TGG ACC CTG GTT AAT GAT GAG ACC Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val Asn Asp Glu Thr 755	760	765		2304
20 CAA GCC AAG ATG GCC CGG ATG GCT GCT GCA GCT GCA TGG GGT TTA GGT Gln Ala Lys Met Ala Arg Met Ala Ala Ala Ala Trp Gly Leu Gly 770	775	780		2352
25 CAG TGG GAC AGC ATG GAA GAA TAC ACC TGT ATG ATC CCT CGG GAC ACC Gln Trp Asp Ser Met Glu Glu Tyr Thr Cys Met Ile Pro Arg Asp Thr 785	790	795	800	2400
30 CAT GAT GGG GCA TTT TAT AGA GCT GTG CTG GCA CTG CAT CAG GAC CTC His Asp Gly Ala Phe Tyr Arg Ala Val Leu Ala Leu His Gln Asp Leu 805	810	815		2448
35 TTC TCC TTG GCA CAA CAG TGC ATT GAC AAG GCC AGG GAC CTG CTG GAT Phe Ser Leu Ala Gln Gln Cys Ile Asp Lys Ala Arg Asp Leu Leu Asp 820	825	830		2496
40 GCT GAA TTA ACT GCA ATG GCA GGA GAG AGT TAC AGT CGG GCA TAT GGG Ala Glu Leu Thr Ala Met Ala Gly Glu Ser Tyr Ser Arg Ala Tyr Gly 835	840	845		2544
45 GCC ATG GTT TCT TGC CAC ATG CTG TCC GAG CTG GAG GAG GTT ATC CAG Ala Met Val Ser Cys His Met Leu Ser Glu Leu Glu Val Ile Gln 850	855	860		2592
50 TAC AAA CTT GTC CCC GAG CGA CGA GAG ATC ATC CGC CAG ATC TGG TGG Tyr Lys Leu Val Pro Glu Arg Arg Glu Ile Ile Arg Gln Ile Trp Trp 865	870	875	880	2640
55 GAG AGA CTG CAG GGC TGC CAG CGT ATC GTA GAG GAC TGG CAG AAA ATC Glu Arg Leu Gln Gly Cys Gln Arg Ile Val Glu Asp Trp Gln Lys Ile 885	890	895		2688
60 CTT ATG GTG CGG TCC CTT GTG GTC AGC CCT CAT GAA GAC ATG AGA ACC Leu Met Val Arg Ser Leu Val Val Ser Pro His Glu Asp Met Arg Thr 900	905	910		2736
65 TGG CTC AAG TAT GCA AGC CTG TGC GGC AAG AGT GGC AGG CTG GCT CTT Trp Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly Arg Leu Ala Leu 915	920	925		2784
70 GCT CAT AAA ACT TTA GTG TTG CTC CTG GGA GTT GAT CCG TCT CGG CAA Ala His Lys Thr Leu Val Leu Leu Gly Val Asp Pro Ser Arg Gln				2832

	930	935	940		
5	CTT GAC CAT CCT CTG CCA ACA GTT CAC CCT CAG GTG ACC TAT GCC TAC Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr Ala Tyr 945	950	955	960	2880
10	ATG AAA AAC ATG TGG AAG AGT GCC CGC AAG ATC GAT GCC TTC CAG CAC Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala Phe Gln His 965	970	975		2928
15	ATG CAG CAT TTT GTC CAG ACC ATG CAG CAA CAG GCC CAG CAT GCC ATC Met Gln His Phe Val Gln Thr Met Gln Gln Ala Gln His Ala Ile 980	985	990		2976
20	GCT ACT GAG GAC CAG CAG CAT AAG CAG GAA CTG CAC AAG CTC ATG GCC Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His Lys Leu Met Ala 995	1000	1005		3024
25	CGA TGC TTC CTG AAA CTT GGA GAG TGG CAG CTG AAT CTA CAG GGC ATC Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn Leu Gln Gly Ile 1010	1015	1020		3072
30	AAT GAG AGC ACA ATC CCC AAA GTG CTG CAG TAC TAC AGC GCC GCC ACA Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr 1025	1030	1035	1040	3120
35	GAG CAC GAC CGC AGC TGG TAC AAG GCC TGG CAT GCG TGG GCA GTG ATG Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met 1045	1050	1055		3168
40	AAC TTC GAA GCT GTG CTA CAC TAC AAA CAT CAG AAC CAA GCC CGC GAT Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp 1060	1065	1070		3216
45	GAG AAG AAG AAA CTG CGT CAT GCC AGC GGG GCC AAC ATC ACC AAC GCC Glu Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala 1075	1080	1085		3264
50	ACC ACT GCC ACC ACG GCC ACT GCC ACC ACC ACT GCC AGC ACC Thr Thr Ala Ala Thr Thr Ala Ala Thr Thr Thr Ala Ser Thr 1090	1095	1100		3312
55	GAG GGC AGC AAC AGT GAG AGC GAG GCC GAG AGC ACC GAG AAC AGC CCC Glu Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro 1105	1110	1115	1120	3360
60	ACC CCA TCG CCG CTG CAG AAG GTC ACT GAG GAT CTG TCC AAA ACC Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys Thr 1125	1130	1135		3408
65	CTC CTG ATG TAC ACG GTG CCT GCC GTC CAG GGC TTC TTC CGT TCC ATC Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg Ser Ile 1140	1145	1150		3456
70	TCC TTG TCA CGA GGC AAC AAC CTC CAG GAT ACA CTC AGA GTT CTC ACC Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg Val Leu Thr 1155	1160	1165		3504

TTA TGG TTT GAT TAT GGT CAC TGG CCA GAT GTC AAT GAG GCC TTA GTG Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu Val 1170 1175 1180	3552
5 GAG GGG GTG AAA GCC ATC CAG ATT GAT ACC TGG CTA CAG GTT ATA CCT Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp Leu Gln Val Ile Pro 1185 1190 1195 1200	3600
10 CAG CTC ATT GCA AGA ATT GAT ACG CCC AGA CCC TTG GTG GGA CGT CTC Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu Val Gly Arg Leu 1205 1210 1215	3648
15 ATT CAC CAG CTT CTC ACA GAC ATT GGT CGG TAC CAC CCC CAG GCC CTC Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His Pro Gln Ala Leu 1220 1225 1230	3696
20 ATC TAC CCA CTG ACA GTG GCT TCT AAG TCT ACC ACG ACA GCC CGG CAC Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr Ala Arg His 1235 1240 1245	3744
25 AAT GCA GCC AAC AAG ATT CTG AAG AAC ATG TGT GAG CAC AGC AAC ACC Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu His Ser Asn Thr 1250 1255 1260	3792
30 CTG GTC CAG CAG GCC ATG ATG GTG AGC GAG GAG CTG ATC CGA GTG GCC Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu Ile Arg Val Ala 1265 1270 1275 1280	3840
35 ATC CTC TGG CAT GAG ATG TGG CAT GAA GGC CTG GAA GAG GCA TCT CGT Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg 1285 1290 1295	3888
40 TTG TAC TTT GGG GAA AGG AAC GTG AAA GGC ATG TTT GAG GTG CTG GAG Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu 1300 1305 1310	3936
45 CCC TTG CAT GCT ATG ATG GAA CGG GGC CCC CAG ACT CTG AAG GAA ACA Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr 1315 1320 1325	3984
50 TCC TTT AAT CAG GCC TAT GGT CGA GAT TTA ATG GAG GCC CAA GAG TGG Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp 1330 1335 1340	4032
55 TGC AGG AAG TAC ATG AAA TCA GGG AAT GTC AAG GAC CTC ACC CAA GCC Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala 1345 1350 1355 1360	4080
TGG GAC CTC TAT TAT CAT GTG TTC CGA CGA ATC TCA AAG CAG CTG CCT Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu Pro 1365 1370 1375	4128
CAG CTC ACA TCC TTA GAG CTG CAA TAT GTT TCC CCA AAA CTT CTG ATG Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met 1380 1385 1390	4176
TGC CGG GAC CTT GAA TTG GCT GTG CCA GGA ACA TAT GAC CCC AAC CAG Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln	4224

	1395	1400	1405	
	CCA ATC ATT CGC ATT CAG TCC ATA GCA CCG TCT TTG CAA GTC ATC ACA			4272
5	Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile Thr			
	1410	1415	1420	
	TCC AAG CAG AGG CCC CGG AAA TTG ACA CTT ATG GGC AGC AAC GGA CAT			4320
	Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His			
10	1425	1430	1435	1440
	GAG TTT GTT TTC CTT CTA AAA GGC CAT GAA GAT CTG CGC CAG GAT GAG			4368
	Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp Glu			
	1445	1450	1455	
15	CGT GTG ATG CAG CTC TTC GGC CTG GTT AAC ACC CTT CTG GCC AAT GAC			4416
	Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn Asp			
	1460	1465	1470	
20	CCA ACA TCT CTT CGG AAA AAC CTC AGC ATC CAG AGA TAC GCT GTC ATC			4464
	Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val Ile			
	1475	1480	1485	
25	CCT TTA TCG ACC AAC TCG GGC CTC ATT GGC TGG GTT CCC CAC TGT GAC			4512
	Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val Pro His Cys Asp			
	1490	1495	1500	
30	ACA CTG CAC GCC CTC ATC CGG GAC TAC AGG GAG AAG AAG AAG ATC CTT			4560
	Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys Lys Lys Ile Leu			
	1505	1510	1515	1520
35	CTC AAC ATC GAG CAT CGC ATC ATG TTG CGG ATG GCT CCG GAC TAT GAC			4608
	Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala Pro Asp Tyr Asp			
	1525	1530	1535	
40	CAC TTG ACT CTG ATG CAG AAG GTG GAG GTG TTT GAG CAT GCC GTC AAT			4656
	His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu His Ala Val Asn			
	1540	1545	1550	
	AAT ACA GCT GGG GAC GAC CTG GCC AAG CTG CTG TGG CTG AAA AGC CCC			4704
45	Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp Leu Lys Ser Pro			
	1555	1560	1565	
	AGC TCC GAG GTG TGG TTT GAC CGA AGA ACC AAT TAT ACC CGT TCT TTA			4752
	Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser Leu			
50	1570	1575	1580	
	GCG GTC ATG TCA ATG GTT GGG TAT ATT TTA GGC CTG GGA GAT AGA CAC			4800
	Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His			
	1585	1590	1595	1600
55	CCA TCC AAC CTG ATG CTG GAC CGT CTG AGT GGG AAG ATC CTG CAC ATT			4848
	Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His Ile			
	1605	1610	1615	
	GAC TTT GGG GAC TGC TTT GAG GTT GCT ATG ACC CGA GAG AAG TTT CCA			4896
	Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe Pro			
	1620	1625	1630	

	GAG AAG ATT CCA TTT AGA CTA ACA AGA ATG TTG ACC AAT GCT ATG GAG Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met Glu 1635 1640 1645	4944
5	GTT ACA GGC CTG GAT GGC AAC TAC AGA ATC ACA TGC CAC ACA GTG ATG Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val Met 1650 1655 1660	4992
10	GAG GTG CTG CGA GAG CAC AAG GAC AGT GTC ATG GCC GTG CTG GAA GCC Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu Ala 1665 1670 1675 1680	5040
15	TTT GTC TAT GAC CCC TTG CTG AAC TGG AGG CTG ATG GAC ACA AAT ACC Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn Thr 1685 1690 1695	5088
20	AAA GGC AAC AAG CGA TCC CGA ACG AGG ACG GAT TCC TAC TCT GCT GGC Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser Tyr Ser Ala Gly 1700 1705 1710	5136
	CAG TCA GTC GAA ATT TTG GAC GGT GTG GAA CTT GGA GAG CCA GCC CAT Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly Glu Pro Ala His 1715 1720 1725	5184
25	AAG AAA ACG GGG ACC ACA GTG CCA GAA TCT ATT CAT TCT TTC ATT GGA Lys Lys Thr Gly Thr Val Pro Glu Ser Ile His Ser Phe Ile Gly 1730 1735 1740	5232
30	GAC GGT TTG GTG AAA CCA GAG GCC CTA AAT AAG AAA GCT ATC CAG ATT Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys Ala Ile Gln Ile 1745 1750 1755 1760	5280
35	ATT AAC AGG GTT CGA GAT AAG CTC ACT GGT CGG GAC TTC TCT CAT GAT Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp Phe Ser His Asp 1765 1770 1775	5328
40	GAC ACT TTG GAT GTT CCA ACG CAA GTT GAG CTG CTC ATC AAA CAA GCG Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Ile Lys Gln Ala 1780 1785 1790	5376
	ACA TCC CAT GAA AAC CTC TGC CAG TGC TAT ATT GGC TGG TGC CCT TTC Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly Trp Cys Pro Phe 1795 1800 1805	5424
45	TGG TAA Trp	5430

50 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met
1 5 10 15

5 Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met
20 25 30

10 Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro
15 35 40 45

Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu
50 55 60

15 Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu
65 70 75 80

20 Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys
85 90 95

25 Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly
100 105 110

Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu
25 115 120 125

Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala
30 130 135 140

35 Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys
145 150 155 160

Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser
165 170 175

35 Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser
180 185 190

40 Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro
195 200 205

Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu
210 215 220

45 Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys
225 230 235 240

50 Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr
245 250 255

Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu
55 260 265 270

Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg
275 280 285

Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu Phe Trp Val Met
290 295 300

Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile Glu Gln Ile Val
305 310 315 320

5 Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro
325 330 335

His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val
340 345 350

10 Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp
355 360 365

15 Asp Tyr Leu His Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala
370 375 380

Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp
385 390 395 400

20 Arg Leu Thr Glu Ser Leu Asp Phe Thr Asp Tyr Ala Ser Arg Ile Ile
405 410 415

His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu Leu Arg Ser Thr
420 425 430

25 Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu Gly Lys Lys Tyr
435 440 445

30 Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val Arg His Arg Ile
450 455 460

Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile Val Lys Gly Tyr
465 470 475 480

35 Thr Leu Ala Asp Glu Glu Asp Pro Leu Ile Tyr Gln His Arg Met
485 490 495

Leu Arg Ser Gly Gln Gly Asp Ala Leu Ala Ser Gly Pro Val Glu Thr
500 505 510

40 Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn Leu Gln Lys Ala
515 520 525

45 Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp Leu Glu Trp Leu
530 535 540

Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser Ser Pro Ser Leu
545 550 555 560

50 Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro Met Ala Arg Asp
565 570 575

Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu Leu Asn Glu Asp
580 585 590

55 Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln
595 600 605

Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu Ala Glu Phe Met
610 615 620

5 Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp Asp Asn Gly Ile
625 630 635 640

Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala Tyr Ala Lys Ala
645 650 655

10 Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro Thr Pro Ala Ile
660 665 670

Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln Gln Pro Glu Ala
675 680 685

15 Ala Ala Gly Val Leu Glu Tyr Ala Met Lys His Phe Gly Glu Leu Glu
690 695 700

20 Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp Glu Asp Ala Leu
705 710 715 720

Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp Asp Pro Glu Leu
725 730 735

25 Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly Glu Trp Gly Gln
740 745 750

Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val Asn Asp Glu Thr
755 760 765

30 Gln Ala Lys Met Ala Arg Met Ala Ala Ala Ala Trp Gly Leu Gly
770 775 780

35 Gln Trp Asp Ser Met Glu Glu Tyr Thr Cys Met Ile Pro Arg Asp Thr
785 790 795 800

His Asp Gly Ala Phe Tyr Arg Ala Val Leu Ala Leu His Gln Asp Leu
805 810 815

40 Phe Ser Leu Ala Gln Gln Cys Ile Asp Lys Ala Arg Asp Leu Leu Asp
820 825 830

Ala Glu Leu Thr Ala Met Ala Gly Glu Ser Tyr Ser Arg Ala Tyr Gly
835 840 845

45 Ala Met Val Ser Cys His Met Leu Ser Glu Leu Glu Val Ile Gln
850 855 860

Tyr Lys Leu Val Pro Glu Arg Arg Glu Ile Ile Arg Gln Ile Trp Trp
50 865 870 875 880

Glu Arg Leu Gln Gly Cys Gln Arg Ile Val Glu Asp Trp Gln Lys Ile
885 890 895

55 Leu Met Val Arg Ser Leu Val Val Ser Pro His Glu Asp Met Arg Thr
900 905 910

Trp Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly Arg Leu Ala Leu

	915	920	925
5	Ala His Lys Thr Leu Val Leu Leu Leu Gly Val Asp Pro Ser Arg Gln 930 935 940		
	Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr Ala Tyr 945 950 955 960		
10	Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala Phe Gln His 965 970 975		
	Met Gln His Phe Val Gln Thr Met Gln Gln Ala Gln His Ala Ile 980 985 990		
15	Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His Lys Leu Met Ala 995 1000 1005		
	Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn Leu Gln Gly Ile 1010 1015 1020		
20	Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr 1025 1030 1035 1040		
	Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met 1045 1050 1055		
25	Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp 1060 1065 1070		
30	Glu Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala 1075 1080 1085		
	Thr Thr Ala Ala Thr Thr Ala Ala Thr Thr Ala Ser Thr Thr Ala Ser Thr 1090 1095 1100		
35	Glu Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro 1105 1110 1115 1120		
	Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys Thr 1125 1130 1135		
40	Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg Ser Ile 1140 1145 1150		
	Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg Val Leu Thr 1155 1160 1165		
45	Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu Val 1170 1175 1180		
50	Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp Leu Gln Val Ile Pro 1185 1190 1195 1200		
	Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu Val Gly Arg Leu 1205 1210 1215		
55	Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His Pro Gln Ala Leu 1220 1225 1230		

Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr Thr Ala Arg His
1235 1240 1245

5 Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu His Ser Asn Thr
1250 1255 1260

Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu Ile Arg Val Ala
1265 1270 1275 1280

10 Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg
1285 1290 1295

Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu
15 1300 1305 1310

Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr
1315 1320 1325

20 Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp
1330 1335 1340

Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala
1345 1350 1355 1360

25 Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu Pro
1365 1370 1375

Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met
30 1380 1385 1390

Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln
1395 1400 1405

35 Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile Thr
1410 1415 1420

Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His
1425 1430 1435 1440

40 Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp Glu
1445 1450 1455

Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn Asp
45 1460 1465 1470

Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val Ile
1475 1480 1485

50 Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val Pro His Cys Asp
1490 1495 1500

Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys Lys Lys Ile Leu
55 1505 1510 1515 1520

Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala Pro Asp Tyr Asp
1525 1530 1535

His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu His Ala Val Asn
1540 1545 1550

Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp Leu Lys Ser Pro
5 1555 1560 1565

Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser Leu
1570 1575 1580

Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His
10 1585 1590 1595 1600

Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His Ile
1605 1610 1615

Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe Pro
15 1620 1625 1630

Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met Glu
20 1635 1640 1645

Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val Met
1650 1655 1660

Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu Ala
25 1665 1670 1675 1680

Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn Thr
1685 1690 1695

Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser Tyr Ser Ala Gly
30 1700 1705 1710

Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly Glu Pro Ala His
35 1715 1720 1725

Lys Lys Thr Gly Thr Val Pro Glu Ser Ile His Ser Phe Ile Gly
1730 1735 1740

Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys Ala Ile Gln Ile
40 1745 1750 1755 1760

Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp Phe Ser His Asp
1765 1770 1775

Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu Ile Lys Gln Ala
45 1780 1785 1790

Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly Trp Cys Pro Phe
50 1795 1800 1805

Trp

55

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

10

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1686

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20

TTG GTT TAC CCT TTG ACA GTT GCT ATT ACT TCC GAA TCA ACG AGC CGT 48
Leu Val Tyr Pro Leu Thr Val Ala Ile Thr Ser Glu Ser Thr Ser Arg
1 5 10 15

25

AAA AAG GCA GCT CAA TCC ATT ATT GAA AAA ATG CGA GTA CAT TCT CCT 96
Lys Lys Ala Ala Gln Ser Ile Ile Glu Lys Met Arg Val His Ser Pro
20 25 30

30

AGC TTG GTG GAT CAA GCA GAA TTA GTG AGT CGA GAA CTC ATC CGA GTT 144
Ser Leu Val Asp Gln Ala Glu Leu Val Ser Arg Glu Leu Ile Arg Val
35 40 45

35

GCA GTT TTA TGG CAC GAA CAA TGG CAC GAT GCT TTG GAA GAT GCT AGC 192
Ala Val Leu Trp His Glu Gln Trp His Asp Ala Leu Glu Asp Ala Ser
50 55 60

40

AGG TTT TTC TTT GGT GAA CAC AAC ACA GAA AAG ATG TTT GAA ACA TTG 240
Arg Phe Phe Phe Gly Glu His Asn Thr Glu Lys Met Phe Glu Thr Leu
65 70 75 80

45

GAA CCA TTA CAT CAA ATG TTG CAA AAG GGA CCA GAA ACG ATG AGG GAA 288
Glu Pro Leu His Gln Met Leu Gln Lys Gly Pro Glu Thr Met Arg Glu
85 90 95

50

CAA GCC TTT GCA AAT GCT TTT GGC AGG GAG TTG ACA GAT GCA TAC GAG 336
Gln Ala Phe Ala Asn Ala Phe Gly Arg Glu Leu Thr Asp Ala Tyr Glu
100 105 110

55

TGG GTG CTC AAC TTT AGA AGA ACT AAA GAC ATA ACC AAT TTG AAT CAA 384
Trp Val Leu Asn Phe Arg Arg Thr Lys Asp Ile Thr Asn Leu Asn Gln
115 120 125

60

GCA TGG GAT ATA TAC TAC AAT GTC TTT AGA AGA GTA AGC AAA CAG GTG 432
Ala Trp Asp Ile Tyr Tyr Asn Val Phe Arg Arg Val Ser Lys Gln Val
130 135 140

65

CAG CTG TTA GCT AGT CTT GAG TTG CAG TAT GTA TCT CCG GAC TTA GAG 480
Gln Leu Leu Ala Ser Leu Glu Leu Gln Tyr Val Ser Pro Asp Leu Glu
145 150 155 160

CAT GCT CAA GAT TTG GAA TTG GCT GTA CCA GGT ACT TAC CAA GCA GGC 528
His Ala Gln Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Gln Ala Gly
165 170 175

	AAA CCT GTG ATC AGA ATA ATC AAA TTT GAT CCT ACT TTT TCG ATT ATT Lys Pro Val Ile Arg Ile Ile Lys Phe Asp Pro Thr Phe Ser Ile Ile 180	185	190	576
5	TCA TCT AAA CAA AGA CCG AGA AAA TTA TCG TGC AGA GGA AGT GAT GGT Ser Ser Lys Gln Arg Pro Arg Lys Leu Ser Cys Arg Gly Ser Asp Gly 195	200	205	624
10	AAA GAC TAC CAA TAT GCG TTG AAA GGA CAT GAA GAT ATC AGA CAA GAT Lys Asp Tyr Gln Tyr Ala Leu Lys Gly His Glu Asp Ile Arg Gln Asp 210	215	220	672
15	AAC TTA GTG ATG CAA TTG TTT GGT TTG GTT AAT ACG TTG TTG GTA AAT Asn Leu Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Val Asn 225	230	235	720
20	GAT CCG GTA TGT TTC AAG AGA CAT TTG GAT ATA CAA CAA TAT CCT GCT Asp Pro Val Cys Phe Lys Arg His Leu Asp Ile Gln Gln Tyr Pro Ala 245	250	255	768
25	ATT CCA TTA TCA CCA AAA GTG GGA TTG CTT GGT TGG GTT CCA AAT AGT Ile Pro Leu Ser Pro Lys Val Gly Leu Leu Gly Trp Val Pro Asn Ser 260	265	270	816
30	GAC ACT TTC CAT GTA TTG ATC AAA GGC TAT CGC GAA TCA AGA AGT ATA Asp Thr Phe His Val Leu Ile Lys Gly Tyr Arg Glu Ser Arg Ser Ile 275	280	285	864
35	ATG TTG AAT ATT GAA CAC AGG CTT TTG TTG CAA ATG GCA CCT GAT TAT Met Leu Asn Ile Glu His Arg Leu Leu Leu Gln Met Ala Pro Asp Tyr 290	295	300	912
40	GAT TTC TTG ACA TTA TTG CAA AAA GTT GAA GTG TTC ACA AGT GCA ATG Asp Phe Leu Thr Leu Leu Gln Lys Val Glu Val Phe Thr Ser Ala Met 305	310	315	960
45	GAT AAT TGT AAG GGA CAG GAT TTG TAC AAA GTG TTA TGG CTC AAA TCT Asp Asn Cys Lys Gly Gln Asp Leu Tyr Lys Val Leu Trp Leu Lys Ser 325	330	335	1008
50	AAA TCA TCC GAG GCG TGG TTG GAC CGT AGA ACA ACA TAC ACG AGA TCA Lys Ser Ser Glu Ala Trp Leu Asp Arg Arg Thr Thr Tyr Thr Arg Ser 340	345	350	1056
55	TTA GCT GTA ATG TCT ATG GTT GGG TAT ATA TTA GGT TTG GGG GAT AGG Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg 355	360	365	1104
55	CAC CCA TCA AAT TTG ATG TTG GAC CGT ATT ACT GGG AAA GTC ATC CAT His Pro Ser Asn Leu Met Leu Asp Arg Ile Thr Gly Lys Val Ile His 370	375	380	1152
55	ATT GAT TTC GGA GAC TGT TTT GAA GCA GCA ATA TTA CGT GAG AAG TAT Ile Asp Phe Gly Asp Cys Phe Glu Ala Ala Ile Leu Arg Glu Lys Tyr 385	390	395	1200
	CCA GAG AGA GTT CCG TTT AGA TTG ACG AGA ATG CTT AAT TAT GCC ATG			1248

405	410	415	
5	GAA GTT AGT GGA ATA GAG GGC TCG TTC AGA ATC ACA TGT GAA CAT GTT Glu Val Ser Gly Ile Glu Gly Ser Phe Arg Ile Thr Cys Glu His Val 420 425 430	1296	
10	ATG AGG GTG TTG CGT GAT AAT AAA GAG TCT TTA ATG GCA ATA TTA GAG Met Arg Val Leu Arg Asp Asn Lys Glu Ser Leu Met Ala Ile Leu Glu 435 440 445	1344	
15	GCC TTT GCT TAC GAT CCC TTG ATA AAT TGG GGG TTT GAT TTC CCA ACA Ala Phe Ala Tyr Asp Pro Leu Ile Asn Trp Gly Phe Asp Phe Pro Thr 450 455 460	1392	
20	AAG GCG TTG GCT GAA TCA ACG GGT ATA CGT GTT CCA CAA GTC AAC ACT Lys Ala Leu Ala Glu Ser Thr Gly Ile Arg Val Pro Gln Val Asn Thr 465 470 475 480	1440	
25	GCA GAA TTA TTA CGC AGA GGA CAG ATT GAC GAA AAA GAA GCT GTA AGA Ala Glu Leu Leu Arg Arg Gly Gln Ile Asp Glu Lys Glu Ala Val Arg 485 490 495	1488	
30	TTG CAA AAG CAA AAT GAA TTG GAA ATA AGA AAC GCT AGA GCT GCA TTA Leu Gln Lys Gln Asn Glu Leu Glu Ile Arg Asn Ala Arg Ala Leu 500 505 510	1536	
35	GTG TTG AAA CGT ATT ACC GAT AAG TTA ACT GGT AAC GAT ATC AAA CGG Val Leu Lys Arg Ile Thr Asp Lys Leu Thr Gly Asn Asp Ile Lys Arg 515 520 525	1584	
40	TTG AGA GGA TTA GAT GTG CCT ACT CAA GTC GAT AAA TTG ATT CAA CAA Leu Arg Gly Leu Asp Val Pro Thr Gln Val Asp Lys Leu Ile Gln Gln 530 535 540	1632	
45	GCC ACC AGT GTT GAG AAT TTG TGT CAG CAT TAC ATT GGT TGG TGT TCG Ala Thr Ser Val Glu Asn Leu Cys Gln His Tyr Ile Gly Trp Cys Ser 545 550 555 560	1680	
50	TGT TGG TAGGTTGATT ATCGTCATGT GTCGATAAGT ATGGTATTGT GGTAACATT Cys Trp	1736	
55	TTATAAAGGG AAATATTAAA GAATTGTATA TTATTAAAAA AAAAAAAA AACTCGAG	1794	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Val Tyr Pro Leu Thr Val Ala Ile Thr Ser Glu Ser Thr Ser Arg

1	5	10	15	
Lys Lys Ala Ala Gln Ser Ile Ile Glu Lys Met Arg Val His Ser Pro				
	20	25	30	
5	Ser Leu Val Asp Gln Ala Glu Leu Val Ser Arg Glu Leu Ile Arg Val			
	35	40	45	
10	Ala Val Leu Trp His Glu Gln Trp His Asp Ala Leu Glu Asp Ala Ser			
	50	55	60	
	Arg Phe Phe Phe Gly Glu His Asn Thr Glu Lys Met Phe Glu Thr Leu			
	65	70	75	80
15	Glu Pro Leu His Gln Met Leu Gln Lys Gly Pro Glu Thr Met Arg Glu			
	85	90	95	
	Gln Ala Phe Ala Asn Ala Phe Gly Arg Glu Leu Thr Asp Ala Tyr Glu			
	100	105	110	
20	Trp Val Leu Asn Phe Arg Arg Thr Lys Asp Ile Thr Asn Leu Asn Gln			
	115	120	125	
25	Ala Trp Asp Ile Tyr Tyr Asn Val Phe Arg Arg Val Ser Lys Gln Val			
	130	135	140	
	Gln Leu Leu Ala Ser Leu Glu Leu Gln Tyr Val Ser Pro Asp Leu Glu			
	145	150	155	160
30	His Ala Gln Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Gln Ala Gly			
	165	170	175	
	Lys Pro Val Ile Arg Ile Ile Lys Phe Asp Pro Thr Phe Ser Ile Ile			
	180	185	190	
35	Ser Ser Lys Gln Arg Pro Arg Lys Leu Ser Cys Arg Gly Ser Asp Gly			
	195	200	205	
40	Lys Asp Tyr Gln Tyr Ala Leu Lys Gly His Glu Asp Ile Arg Gln Asp			
	210	215	220	
	Asn Leu Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Val Asn			
	225	230	235	240
45	Asp Pro Val Cys Phe Lys Arg His Leu Asp Ile Gln Gln Tyr Pro Ala			
	245	250	255	
	Ile Pro Leu Ser Pro Lys Val Gly Leu Leu Gly Trp Val Pro Asn Ser			
	260	265	270	
50	Asp Thr Phe His Val Leu Ile Lys Gly Tyr Arg Glu Ser Arg Ser Ile			
	275	280	285	
55	Met Leu Asn Ile Glu His Arg Leu Leu Leu Gln Met Ala Pro Asp Tyr			
	290	295	300	
	Asp Phe Leu Thr Leu Leu Gln Lys Val Glu Val Phe Thr Ser Ala Met			
	305	310	315	320

Asp Asn Cys Lys Gly Gln Asp Leu Tyr Lys Val Leu Trp Leu Lys Ser
325 330 335

5 Lys Ser Ser Glu Ala Trp Leu Asp Arg Arg Thr Thr Tyr Thr Arg Ser
340 345 350

Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg
355 360 365

10 His Pro Ser Asn Leu Met Leu Asp Arg Ile Thr Gly Lys Val Ile His
370 375 380

Ile Asp Phe Gly Asp Cys Phe Glu Ala Ala Ile Leu Arg Glu Lys Tyr
15 385 390 395 400

Pro Glu Arg Val Pro Phe Arg Leu Thr Arg Met Leu Asn Tyr Ala Met
405 410 415

20 Glu Val Ser Gly Ile Glu Gly Ser Phe Arg Ile Thr Cys Glu His Val
420 425 430

Met Arg Val Leu Arg Asp Asn Lys Glu Ser Leu Met Ala Ile Leu Glu
435 440 445

25 Ala Phe Ala Tyr Asp Pro Leu Ile Asn Trp Gly Phe Asp Phe Pro Thr
450 455 460

Lys Ala Leu Ala Glu Ser Thr Gly Ile Arg Val Pro Gln Val Asn Thr
30 465 470 475 480

Ala Glu Leu Leu Arg Arg Gly Gln Ile Asp Glu Lys Glu Ala Val Arg
485 490 495

35 Leu Gln Lys Gln Asn Glu Leu Glu Ile Arg Asn Ala Arg Ala Ala Leu
500 505 510

Val Leu Lys Arg Ile Thr Asp Lys Leu Thr Gly Asn Asp Ile Lys Arg
515 520 525

40 Leu Arg Gly Leu Asp Val Pro Thr Gln Val Asp Lys Leu Ile Gln Gln
530 535 540

Ala Thr Ser Val Glu Asn Leu Cys Gln His Tyr Ile Gly Trp Cys Ser
45 545 550 555 560

Cys Trp

50 (2) INFORMATION FOR SEQ ID NO:15:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

5 (A) NAME/KEY: CDS
(B) LOCATION: 1..399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

10	GT	TT	AG	T	AG	GT	CA	C	AC	G	AG	TT	AT	TC	AG	GA	GT	CT	TA	TG	CA	G	AA	TT	TA	TG	48	
	Val	Ser	His	Glu	Leu	Ile	Arg	Val	Ala	Val	Leu	Trp	His	Glu	Leu	Trp												
	1				5					10											15							
15	TA	T	AT	GA	GG	CT	GA	GA	GAT	GCG	AGC	CGC	CA	TT	TT	TC	GT	GA	CA	T	AAC							96
	Tyr	Glu	Gly	Leu	Glu	Gly	Leu	Glu	Asp	Ala	Ser	Arg	Gln	Phe	Phe	Val	Glu	His	Asn									
					20						25										30							
20	AT	AT	AA	AA	AT	GG	TT	TT	CT	AC	TT	GA	CC	TT	CA	AA	CA	TT	GG								144	
	Ile	Glu	Lys	Met	Phe	Ser	Thr	Leu	Glu	Pro	Leu	His	Lys	His	Leu	Gly												
					35					40											45							
25	AA	AT	AG	CT	CA	AC	TT	AG	GA	TC	TT	CAG	AA	TC	TT	GG										192		
	Asn	Glu	Pro	Gln	Thr	Leu	Ser	Glu	Val	Ser	Phe	Gln	Lys	Ser	Phe	Gly												
					50					55											60							
30	AG	GA	TT	AA	GAT	GCC	TAC	GA	TT	G	AG	GT	TC	TT	CAG	AA	TC	TT	GG								240	
	Arg	Asp	Leu	Asn	Asp	Ala	Tyr	Glu	Trp	Leu	Asn	Asn	Tyr	Lys	Lys	Ser												
					65					70											75							80
35	AA	GAC	ATC	AAT	AAT	TT	GA	CA	GCT	TG	GAT	AT	T	T	T	T	AAC	GTC								288		
	Lys	Asp	Ile	Asn	Asn	Leu	Asn	Gln	Ala	Trp	Asp	Ile	Tyr	Tyr	Asn	Val												
					85					90											95							
40	TT	CA	GA	AA	AT	AC	CG	CA	AT	CC	CA	G	TT	CA	AC	TT	GA	CT	GA	TT	G	CT	GA	TT	G	384		
	CAG	CAT	GTT	TCT	CCC	CAG	CTT	CTG	GCT	ACT	CAT	GAT	CTC	GAA	TT	GCT												
	Gln	His	Val	Ser	Pro	Gln	Leu	Leu	Ala	Thr	His	Asp	Leu	Glu	Leu	Ala												
					115					120											125							
45	GT	TT	CCT	GG	AC	CA	TAT																				399	
	Val	Pro	Gly	Thr	Tyr																							
					130																							

(2) INFORMATION FOR SEQ ID NO:16:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Ser His Glu Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp
1 5 10 15

Tyr Glu Gly Leu Glu Asp Ala Ser Arg Gln Phe Phe Val Glu His Asn
5 20 25 30

Ile Glu Lys Met Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly
35 40 45

10 Asn Glu Pro Gln Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly
50 55 60

Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Lys Ser
65 70 75 80

15 Lys Asp Ile Asn Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
85 90 95

20 Phe Arg Lys Ile Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu
100 105 110

Gln His Val Ser Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala
115 120 125

25 Val Pro Gly Thr Tyr
130

30 (2) INFORMATION FOR SEQ ID NO:17:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

45 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..399

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTC AGC CAC GAA TTG ATA CGT ATG GCG GTG CTT TGG CAT GAG CAA TGG
Val Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp
1 5 10 15

48

50 TAT GAG GGT CTG GAT GAC GCC AGT AGG CAG TTT TTT GGA GAA CAT AAT
Tyr Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn
20 25 30

96

55 ACC GAA AAA ATG TTT GCT GCT TTA GAG CCT CTG TAC GAA ATG CTG AAG
Thr Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys
35 40 45

144

AGA GGA CCG GAA ACT TTG AGG GAA ATA TCG TTC CAA AAT TCT TTT GGT	192
Arg Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly	
50 55 60	
5 AGG GAC TTG AAT GAC GCT TAC GAA TGG CTG ATG AAT TAC AAA AAA TCT	240
Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser	
65 70 75 80	
10 AAA GAT GTT AGT AAT TTA AAC CAA GCG TGG GAC ATT TAC TAT AAT GTT	288
Lys Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val	
85 90 95	
15 TTC AGG AAA ATT GGT AAA CAG TTG CCA CAA TTA CAA ACT CTT GAA CTA	336
Phe Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu	
100 105 110	
20 CAA CAT GTG TCG CCA AAA CTA CTA TCT GCG CAT GAT TTG GAA TTG GCT	384
Gln His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala	
115 120 125	
25 GTC CCC GGG ACC CGT	399
Val Pro Gly Thr Arg	
130	
30 (2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS:	
35 (A) LENGTH: 133 amino acids	
(B) TYPE: amino acid	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
Val Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp	
1 5 10 15	
40 Tyr Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn	
20 25 30	
45 Thr Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys	
35 40 45	
45 Arg Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly	
50 55 60	
50 Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser	
65 70 75 80	
55 Lys Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val	
85 90 95	
55 Phe Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu	
100 105 110	
Gln His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala	

115

120

125

Val Pro Gly Thr Arg
130

5

(2) INFORMATION FOR SEQ ID NO:19:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGACCCTCAC	CCCTTCCACC	TATCCAAAAA	ACCTCACTGG	GTCTGTGGAC	AAACAACANA	60
AATNTTTTCC	ANANAGGCC	CAAATGAGNC	CCANGGTCT	NTCTTCCATC	AGACCCAGTG	120
25 ATTCTGCGAC	TCACACNCTT	CAATTCAAGA	CCTGACCNC	AGTAGGGAGG	TTTANTCAGA	180
TCGCTGGCAN	CCTCGGCTGA	NCAGATNCAN	AGNGGGNTC	GCTGTTCA	GGGNCCACCC	240
30 TCNCTGGCCT	TCTTCANCAG	GGGTCTGGGA	TGTTTCAGT	GGNCCNAANA	CNCTGTTAG	300
AGCCAGGGCT	CAGNAAACAG	AAAANCTNTC	ATGGNGGTT	TGGACACAGG	GNAGGTCTGG	360
NACATATTGG	GGATTATGAN	CAGNACCAAN	ACNCCACTAA	ATNCCCCAAG	NANAAAGTGT	420
35 AACCATNTCT	ANACNCCATN	TTNTATCAGN	ANAAATT	TTCCNATAAA	TGACATCAGN	480
ANTTTNAACA	TNAAAAAAA	AAAAAAA	AAAANAAAAA	AAAAAAA	A	531

40 (2) INFORMATION FOR SEQ ID NO:20:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 128
(D) OTHER INFORMATION: /label= XhoI

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5 GCGTATAACG CGTTTGGAAT CACTACAGGG ATGTTAATA CCACTACAAT GGATGATGTA 60
TATAACTATC TATTCGATGA TGAAGATACC CCACCAAACC CAAAAAAAGA GATCTGGAAT 120
TCGGATCCTC GAGAGATCTA TGAATCGTAG ATACTGAAAA ACCCGCAAG TTCACTCAA 180
CTGTGCATCG TGCACCATCT CAATTCTTT CATTATACA TCGTTTGCC T 231

10 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

25 TGAAGATACC CCACCAAACC C

21

25 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

40 TGCACAGTTG AAGTGAAC

18

45 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 662 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: both
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 60..416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	ACCAAACCCA AAAAAAGAGA TCCTAGNAAC TAGTGGATCC CCCGGGCTGC AGGAATTG	59
5	GTA CGA GTC GCC CTC AGC AGA CTC GCC CAG GAG AGG AAA GCA TGG AGG Val Arg Val Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg 1 5 10 15	107
10	AAA GAC CAC CCA TTT GGT TTC GTG GCT GTC CCA ACA AAA AAT CCC GAT Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp 20 25 30	155
15	GGC ACG ATG AAC CTC ATG AAC TGG GAG TGC GCC ATT CCA GGA AAG AAA Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys 35 40 45	203
20	GGG ACT CCG TGG GAA GGA GGC TTG TTT AAA CTA CGG ATG CTT TTC AAA Gly Thr Pro Trp Glu Gly Leu Phe Lys Leu Arg Met Leu Phe Lys 50 55 60	251
25	GAT GAT TAT CCA TCT TCG CCA CCA AAA TGT AAA TTC GAA CCA CCA TTA Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu 65 70 75 80	299
30	TTT CAC CCG AAT GTG TAC CCT TCG GGG ACA GTG TGC CTG TCC ATC TTA Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu 85 90 95	347
35	GAG GAG GAC AAG GAC TGG AGG GCA GNC ATC ACA ATC AAA CAG GAT CCT Glu Glu Asp Lys Asp Trp Arg Ala Xaa Ile Thr Ile Lys Gln Asp Pro 100 105 110	395
40	ATT AGG AAT ACA GGA ACT TTC TAAATGAACC AAATATCCAA GACCAGNTCA Ile Arg Asn Thr Gly Thr Phe 115	446
45	AGCAGAGGGC TACANGATT ACTGCCAAA CAGAGTNGNG TACGAGAAAG GGTCCGAGCA NAGCCAGAAG TTTGGGCCTC ATTAGCAGGG ACCTGGTGA TCGTCAAAGG AGGTTTGGTT GGGAAGACTT GTTCAANATT TNGGAANTTA AGTTGTCCNN NAACTNGCGG GGGGGGGNNN NNCNNTTNC CANTTCCCTN CCCCCNGTTT TTNGNT	506 566 626 662

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids
50 (B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Val Arg Val Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg
1 5 10 15

Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp
20 25 30

5 Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys
35 40 45

Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe Lys
50 55 60

10 Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu
65 70 75 80

Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu
15 85 90 95

Glu Glu Asp Lys Asp Trp Arg Ala Xaa Ile Thr Ile Lys Gln Asp Pro
100 105 110

20 Ile Arg Asn Thr Gly Thr Phe
115

(2) INFORMATION FOR SEQ ID NO:25:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCCTCCCTCC TGCCGCTCCT CTCTAGAACCC TTCTAGAACCC TGGGCTGTGC TGCTTTGAG 60
40 CCTCAGACCC CAGGGCAGCA TCTCGGTTCT GCGCCACTTC CTTTGTGTTT ANATGGCGTT 120
TTGTCTGTGT TGCTGTTAG AGTAGATNAA CTGTTTANAT AAAAAAAA NAAAATTNAC 180
45 TNGAGGGGGC NTGNAGGCAT GCNNAAC 207